

## SEQUENCE LISTING

<110> DSM IP ASSETS BV  
Institute National de la Recherche Agronomique

<120> YEAST STRAINS WITH IMPROVED FRUCTOSE FERMENTATION CAPACITY

<130> 21568WO

<150> EP 03078992.9  
<151> 2003-12-19

<160> 30

<170> PatentIn version 3.1

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&lt;210&gt; 26

&lt;211&gt; 567

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 26

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20	25	30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val		
35	40	45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile		
50	55	60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr			
65	70	75	80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe		
85	90	95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr		
100	105	110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile  
115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile  
130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Gln Ile Ala Ser  
145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu  
165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val  
180 185 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met  
195 200 205

Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys  
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe  
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser  
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser  
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln  
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly  
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys  
305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly  
325 330 335

Asp Asn Tyr Phe Phe Tyr Gly Thr Thr Val Phe Asn Ala Val Gly

340

345

350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe  
355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg  
370 375 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val  
385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn  
405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe  
420 425 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val  
435 440 445

Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile  
450 455 460

Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr  
465 470 475 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met  
485 490 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Val Pro Glu  
500 505 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly  
515 520 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly  
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Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr  
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Lys Lys Met Phe Gly Lys Lys  
565

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<213> Mutated HXT3 protein

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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val  
35 40 45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile  
50 55 60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr  
65 70 75 80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe  
85 90 95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr  
100 105 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile  
115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile  
130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser  
145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu  
165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val  
180 185 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met  
195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys  
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe  
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser  
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser  
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln  
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly  
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys  
305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly  
325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly  
340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe  
355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg  
370 375 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val  
385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn  
405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe

11/16

420

425

430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val  
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Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile  
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Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met  
 485                   490                   495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Val Pro Glu  
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Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly  
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Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly  
 530                   535                   540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr  
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Lys Lys Met Phe Gly Lys Lys  
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ggtaccattt ctggttcgt cgcccaaact gatttcttga gaagattcgg tatgaagcat	300	
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gtcaatgata tgcgtgtt ggtgttctt ccatgaaatgtt ctgcttgcata ggttccaaaca	1620
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aagaaaatgtt tcggcaagaa ataa	1704

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120

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&lt;212&gt; PRT

&lt;213&gt; Mutated HXT3 protein II

&lt;400&gt; 30

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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro  
20 25 30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val  
35 40 45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile  
50 55 60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr  
65 70 75 80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe  
85 90 95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr  
100 105 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile  
115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile  
130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser  
145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu  
165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val  
180 185 190

Ala Pro Lys Glu Met Arg Gly Ala Leu Val Ser Cys Tyr Gln Leu Met  
195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys  
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe  
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser  
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser  
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln  
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly  
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys  
305 310 315 320

Arg Thr Met Ile Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly  
325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly  
340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe  
355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg  
370 375 380

Asn Cys Leu Met Trp Gly Ala Val Gly Met Val Cys Cys Tyr Val Val  
385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Gln Asn Asn  
405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe  
420 425 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val

435

440

445

Val Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile  
450 455 460

Ala Thr Ala Ala Asn Trp Ile Trp Gly Phe Leu Ile Gly Phe Phe Thr  
465 470 475 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met  
485 490 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Val Pro Glu  
500 505 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly  
515 520 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly  
530 535 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr  
545 550 555 560

Lys Lys Met Phe Gly Lys Lys  
565